

CLAIMS:

1. A method for indicating the likelihood that a DNA mixture arose from sources of a defined type where the DNA mixture is formed by DNA samples from more than one source, the method involving:-

the determination of the identity of the alleles present at a locus for the DNA in the mixture;

determining a first probability function for the situation where the DNA mixture is formed from samples arising from the given person and from a first other person;

determining a second probability function for the situation where the DNA mixture is formed from samples arising from a second other person and a first other person;

using the first probability function as numerator and the second probability function as denominator in determining a likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function;

determining such likelihood ratios for a plurality of loci; and

combining the likelihood ratios to give a combined likelihood ratio for the mixture having arisen from the defined type of sources considered in the first probability function.

2. A method according to claim 1 in which the first probability function is the probability that the defined type provides one or both of the mixture sources based on the frequency of occurrence of the possible allele combinations which could generate the identified allele identity or identities for that locus.

3. A method according to claim 1 in which the second probability function is the probability that the first and second other persons provide the identity for the mixture sources based on the frequency of occurrence of possible allele combinations which could have generated the identified allele identity of identities for that locus.

4. A method according to claim 1 where the defined type is the given person and an unknown person, the first function is based on the frequency of occurrence of the different possible allele combinations for the unknown person which are possible knowing the given persons alleles at that locus.
5. A method according to claim 1 where the defined type is the given person and an unknown person, the second function is based on the frequency of occurrence of the different allele combinations which are possible from the two unknown persons which give the allele identity or identities obtained.
6. A method according to claim 1 where the defined type is the given person and the first other person is a known person, the first function is defined as 1.
7. A method according to claim 1 where the defined type is the given person and the first other person is a known person, the second function is based on the frequency of occurrence of the different possible allele combinations for the unknown person which are possible knowing the known person's alleles at that locus.
8. A method according to claim 1 in which the method is applied to at least 20 loci.
9. A method according to claim 1 in which the combined likelihood ratio is obtained by multiplying the individual likelihood ratios together.
10. A method according to claim 1 in which to estimate the optimum number of loci used a theoretical likelihood ratio is used, calculated from:-

$$\overline{LR}_n = \prod_{m=1}^{mp} LR^{(fm \times n)}$$

where n is the number of loci; m_p is the number of possible allele identities for a simple mixture; LR is the likelihood ratio; LR is the combined likelihood ratio; and f_m is the proportion of an array of a loci having a particular mixture type m .

11. A method according to claim 1 where the allele identity or identities of a given person and/or known first other person are under consideration, the method includes the determination of the allele identity or identities at one or more of the loci under consideration from DNA obtained only from the given person or known first person.
12. A method according to claim 1 where the defined type is the given person and the first other person is a known person, such as a victim, and at least some of the loci considered in the method are those in which the given person and first other person are known to differ in allele identity.
13. A method according to claim 1 where the defined type is the given person and the first other person is a known person, such as a victim, the method considers loci at which the given person and known first person are known to have the same homozygous allele identity.
14. A method according to claim 13 in which in such cases the method includes the establishment of a probability value that the other identity is absent.
15. A method according to claim 13 in which the probability value involves an investigation of the background noise level from the allele identity investigating process and / or the introduction of one or more negative control samples and / or the determination of a cumulative probability density function for one or more or all of the negative controls.
16. A method according to claim 1 where the defined type is the given person and the first other person is a known person, such as a victim, the method involves the establishment of a probability value that the given person's allele identity or identities has not been detected.

17. A method according to claim 16 in which the probability value relates to the given person's allele identity being different from that of the known first other person's.
18. A method according to claim 16 in which the probability value relates to the given person's allele identity being the same as that of the known first other person's.
19. A method according to claim 1 in which the method further includes the prediction of the proportion of the mixture arising from the person other than the first other person, for instance from the suspect as the given person.
20. A method according to claim 1 in which the method includes an estimate or calculation of a value for $p(\text{null})$, the value for $p(\text{null})$ being calculated from a cumulative probability density function.

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